

WHAT IS CLAIMED IS:

1 1. An isolated nucleic acid sequence encoding a microtubule motor
 2 protein, wherein the protein has the following properties:
 3 (i) the protein's activity includes plus end-directed microtubule motor activity; and
 4 (ii) the protein has a tail domain that has greater than 60% amino acid sequence
 5 identity to a TL- γ tail domain as measured using a sequence comparison algorithm.

1 2. An isolated nucleic acid sequence of claim 1, wherein the protein
 2 specifically binds to polyclonal antibodies to TL- γ .

1 3. An isolated nucleic acid sequence of claim 1, wherein the nucleic
 2 acid encodes TL- γ .

1 4. An isolated nucleic acid sequence of claim 1, wherein the nucleic
 2 acid encodes SEQ ID NO:1 (AA seq)

1 5. An isolated nucleic acid sequence of claim 1, wherein the nucleic
 2 acid has a nucleotide sequence of SEQ ID NO:2.

1 6. An isolated nucleic acid sequence of claim 1, wherein the sequence
 2 comparison algorithm is PILEUP.

1 7. An isolated nucleic acid sequence of claim 1, wherein the nucleic
 2 acid is amplified by primers that selectively hybridize under stringent hybridization
 3 conditions to the same sequence as the primer set:

5' ATGTCGGGCGGTGGAAATATC 3' (SEQ ID NO:3)

5' GAATTCCTGCTTCGCTGTTTCA 3' (SEQ ID NO:4)

1 8. An isolated nucleic acid sequence of claim 1, wherein the nucleic
 2 acid has identity to a TL- γ derived from a hyphal fungi.

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1 9. An isolated nucleic acid sequence of claim 8, wherein the nucleic
 2 acid has identity to a TL- γ derived from *Thermomyces lanuginosus*.

1 10. An isolated nucleic acid sequence of claim 1, wherein the nucleic
 2 acid selectively hybridizes under stringent hybridization conditions to SEQ ID NO:2.

1 11. An expression vector comprising a nucleic acid encoding a
 2 microtubule motor protein, wherein the protein has the following properties:

- 3 (i) the protein's activity includes plus end-directed microtubule motor activity; and
 4 (ii) the protein has a tail domain that has greater than 60% amino acid sequence
 5 identity to a TL- γ tail domain, as measured using a sequence comparison algorithm.

1 12. A expression vector of claim 11, wherein the protein specifically
 binds to polyclonal antibodies to TL- γ .

1 13. A host cell transfected with the vector of claim 11.

1 14. An isolated microtubule motor protein, wherein the protein has the
 2 following properties:

- 3 (i) the protein's activity includes plus end-directed microtubule motor activity; and
 4 (ii) the protein has a tail domain that has greater than 60% amino acid sequence
 5 identity to a TL- γ core tail domain as measured using a sequence comparison algorithm.

1 15. An isolated protein of claim 14, wherein the protein specifically
 2 binds to polyclonal antibodies to TL- γ .

1 16. An isolated protein of claim 14, wherein the protein is TL- γ .

1 17. An isolated protein of claim 14, wherein the protein has an amino
 2 acid sequence of SEQ ID NO:1.

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1 28. An antibody of claim 23, wherein the antibody is a chimeric
2 antibody.

1 29. A method for diagnosing hyphal fungal infections by detecting the
2 presence of TL- γ in a sample, the method comprising the steps of:

3 (i) obtaining a biological sample;

4 (ii) contacting the biological sample with a TL- γ specific reagent that selectively
5 associates with TL- γ ; and,

6 (iii) detecting the level of TL- γ specific reagent that selectively associates with the
7 sample.

1 30. A method of claim 29, wherein the TL- γ specific reagent is selected
2 from the group consisting of: TL- γ specific antibodies, TL- γ specific oligonucleotide
3 primers, and TL- γ nucleic acid probes.

1 31. A method of claim 29, wherein the sample is from a human.

1 32. A method of claim 29, wherein the sample is from an animal.

1 33. A method of claim 29, wherein the TL- γ specific reagent is part of
2 a gene or protein array.

1 34. A method for screening for modulators of TL- γ , the method
2 comprising the steps of:

3 (i) providing biologically active TL- γ , wherein the TL- γ has the following
4 properties

5 (a) the protein's activity includes plus end-directed microtubule motor
6 activity; and

7 (b) the protein has a tail domain that has greater than 60% amino acid
8 sequence identity to a TL- γ tail domain as measured using a sequence comparison
9 algorithm;

10 (ii) contacting biologically active TL- γ with a candidate agent in a test and control
11 concentration; and

1 (iii) assaying for the level of TL- γ activity, wherein the TL- γ activity plus end-
2 directed microtubule motor activity, binding activity or ATPase activity, and wherein a
3 change in activity between the test and control concentration indicates a modulator.

1 35. A method of claim 34, wherein the protein specifically binds to
2 polyclonal antibodies to TL- γ .

1 36. A method of claim 34, further comprising the step of isolating
2 biologically active TL- γ from a cell sample.

1 37. A method of claim 34, wherein the biologically active TL- γ is
2 recombinant.

1 38. A method of claim 34, wherein the biologically active TL- γ has
2 identity to a TL- γ derived from *Thermomyces lanuginosus*.

1 39. A method of claim 34, wherein the candidate agent is selected from
2 the group consisting of antibodies, proteins, oligonucleotides and small molecules.

1 40. A method of claim 34, wherein the screening occurs in a multi-well
2 plate as part of a high-throughput screen.

1 41. A method of claim 34, wherein the biologically active TL- γ
2 comprises a motor domain having identity to the motor domain of *Thermomyces*
3 *lanuginosus* TL- γ .

1 42. A method of claim 34, wherein the biologically active TL- γ
2 comprises an amino acid sequence of a TL- γ motor domain of SEQ ID NO:1.

1 43. A kit for screening for modulators of TL- γ , the kit comprising;
2 (i) a container holding biologically active TL- γ ; and

1 (ii) instructions for assaying for TL- γ activity, wherein the TL- γ activity is
2 plus end-directed microtubule motor activity, binding activity, or ATPase activity.

1 44. A kit of claim 43, wherein the biologically active TL- γ has identity
2 to a TL- γ derived from *Thermomyces lanuginosus*.

1 45. A kit of claim 43, wherein the biologically active TL- γ comprises a
2 motor domain that has identity to the motor domain of *Thermomyces lanuginosus* TL- γ .

1 46. A kit of claim 43, wherein the biologically active TL- γ is
2 recombinant.

1 47. In a computer system, a method of screening for mutations of
2 microtubule motor protein genes, the method comprising the steps of:

3 (i) entering at least 30 nucleotides of a first nucleic acid sequence encoding a plus
4 end-directed microtubule motor protein having a nucleotide sequence of SEQ ID NO:2
5 and conservatively modified versions thereof;

6 (ii) comparing the first nucleic acid sequence with a second nucleic acid sequence
7 having substantial identity to the first nucleic acid sequence; and

8 (iii) identifying nucleotide differences between the first and second nucleic acid
9 sequences.

1 48. In a computer system, a method for identifying a three-dimensional
2 structure of microtubule motor proteins, the method comprising the steps of:

3 (i) entering an amino acid sequence of at least 10 amino acids of a plus
4 end-directed microtubule motor protein or a nucleotide sequence of at least 30 nucleotides
5 of a gene encoding the motor protein, the protein having an amino acid sequence of SEQ
6 ID NO:1 and conservatively modified versions thereof; and

7 (ii) generating a three-dimensional structure of the protein encoded by the
8 amino acid sequence.

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ntity with SEQ ID NO

50. An isolated nucleic acid has the same base sequence and base pairing identity with nucleotides

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1 52. An isolated nucleic acid comprising a sequence which has greater
2 than 60% sequence identity with nucleotides 1804-2352 of SEQ ID NO:2.

53. An isolated nucleic acid sequence
to a complement of SEQ ID NO:2.

54. An isolated nucleic acid sequence which hybridizes under stringent conditions to a complement of nucleotides 1-1071 of SEQ ID NO:2.

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56. An isolated nucleic acid sequence which hybridizes under stringent conditions to a complement of nucleotides 1804-2352 of SEQ ID NO:2.

57. An method for identifying sequence changes among homologs
sequencing the nucleic acid of any one of claims 49-53 and identifying
changes compared to the corresponding sequence of SEQ ID NO:2.

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